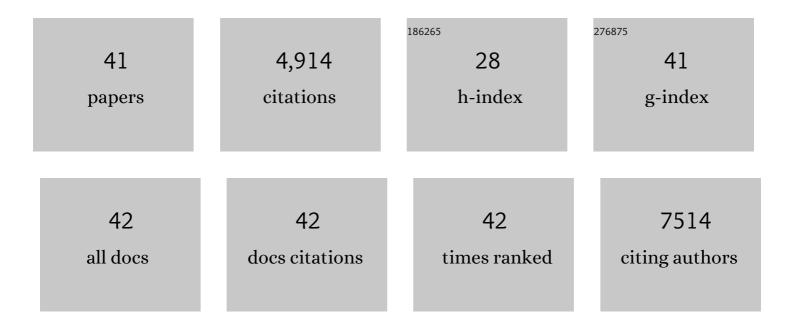
Felipe Rodrigues da Silva

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Transcriptomic analysis related to the flowering of the citrus hybrid Microcitrangemonia. Current Plant Biology, 2019, 18, 100097.	4.7	1
2	In vitro and in silico validation of CA3 and FHL1 downregulation in oral cancer. BMC Cancer, 2018, 18, 193.	2.6	6
3	Generation of iPSC-Derived Human Peripheral Sensory Neurons Releasing Substance P Elicited by TRPV1 Agonists. Frontiers in Molecular Neuroscience, 2018, 11, 277.	2.9	33
4	<i>S</i> â€nitrosoglutathione promotes cell wall remodelling, alters the transcriptional profile and induces root hair formation in the hairless <i>root hair defective 6</i> (<i>rhd6</i>) mutant of <i>Arabidopsis thaliana</i> . New Phytologist, 2017, 213, 1771-1786.	7.3	23
5	First Report of <i>Papaya ringspot virus-</i> Type W Infecting <i>Fevillea</i> Species (Cucurbitaceae) in South America. Plant Disease, 2016, 100, 2540-2540.	1.4	2
6	InteractiVenn: a web-based tool for the analysis of sets through Venn diagrams. BMC Bioinformatics, 2015, 16, 169.	2.6	1,609
7	Transcriptome analysis highlights changes in the leaves of maize plants cultivated in acidic soil containing toxic levels of Al3+. Molecular Biology Reports, 2014, 41, 8107-8116.	2.3	26
8	Sugarcane genome sequencing by methylation filtration provides tools for genomic research in the genus <i><scp>S</scp>accharum</i> . Plant Journal, 2014, 79, 162-172.	5.7	40
9	Identification of upregulated genes in oral squamous cell carcinomas. Head and Neck, 2013, 35, 1475-1481.	2.0	35
10	Differentially expressed genes and proteins upon drought acclimation in tolerant and sensitive genotypes of Coffea canephora. Journal of Experimental Botany, 2012, 63, 4191-4212.	4.8	72
11	Linking microarray data to QTLs highlights new genes related to Al tolerance in maize. Plant Science, 2012, 191-192, 8-15.	3.6	10
12	A BAC library of the SP80-3280 sugarcane variety (saccharum sp.) and its inferred microsynteny with the sorghum genome. BMC Research Notes, 2012, 5, 185.	1.4	47
13	Expressed sequence-tag analysis of ovaries of Brachiaria brizantha reveals genes associated with the early steps of embryo sac differentiation of apomictic plants. Plant Cell Reports, 2012, 31, 403-416.	5.6	28
14	An EST-based analysis identifies new genes and reveals distinctive gene expression features of Coffea arabica and Coffea canephora. BMC Plant Biology, 2011, 11, 30.	3.6	67
15	Spinning Gland Transcriptomics from Two Main Clades of Spiders (Order: Araneae) - Insights on Their Molecular, Anatomical and Behavioral Evolution. PLoS ONE, 2011, 6, e21634.	2.5	30
16	A Study of Gene Expression in the Nematode Resistant Wild Peanut Relative, Arachis stenosperma, in Response to Challenge with Meloidogyne arenaria. Tropical Plant Biology, 2010, 3, 183-192.	1.9	30
17	Transcriptional profile of maize roots under acid soil growth. BMC Plant Biology, 2010, 10, 196.	3.6	51
18	Selection of reference genes for quantitative real-time PCR expression studies in the apomictic and sexual grass Brachiaria brizantha. BMC Plant Biology, 2009, 9, 84.	3.6	118

#	Article	IF	CITATIONS
19	Identification of drought-responsive genes in roots of upland rice (Oryza sativa L). BMC Genomics, 2008, 9, 485.	2.8	104
20	Insights into the Musa genome: Syntenic relationships to rice and between Musa species. BMC Genomics, 2008, 9, 58.	2.8	105
21	Spidroins from the Brazilian spider Nephilengys cruentata (Araneae: Nephilidae). Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2007, 147, 597-606.	1.6	22
22	ESTs from a wild Arachis species for gene discovery and marker development. BMC Plant Biology, 2007, 7, 7.	3.6	112
23	Molecular detection of Papaya meleira virus in the latex of Carica papaya by RT-PCR. Journal of Virological Methods, 2007, 146, 305-310.	2.1	27
24	Identification and characterization of a resistance gene analog (RGA) from the Caricaceae Dumort family. Revista Brasileira De Fruticultura, 2006, 28, 458-462.	0.5	2
25	Brazilian coffee genome project: an EST-based genomic resource. Brazilian Journal of Plant Physiology, 2006, 18, 95-108.	0.5	112
26	Analysis of expressed sequence tags from Musa acuminata ssp. burmannicoides, var. CalcuttaÂ4 (AA) leaves submitted to temperature stresses. Theoretical and Applied Genetics, 2005, 110, 1517-1522.	3.6	30
27	Endosperm-preferred Expression of Maize Genes as Revealed by Transcriptome-wide Analysis of Expressed Sequence Tags. Plant Molecular Biology, 2005, 59, 363-374.	3.9	28
28	Nucleotide sequence and phylogenetic analyses of the DNA polymerase gene of Anticarsia gemmatalis nucleopolyhedrovirus. Virus Research, 2005, 110, 99-109.	2.2	2
29	Evaluation of Monocot and Eudicot Divergence Using the Sugarcane Transcriptome. Plant Physiology, 2004, 134, 951-959.	4.8	38
30	The mitochondrial genome of the blowfly Chrysomya chloropyga (Diptera: Calliphoridae). Gene, 2004, 339, 7-15.	2.2	151
31	Overexpression, purification, biochemical characterization, and molecular modeling of recombinant GDP-mannosyltransferase (GumH) from Xylella fastidiosa. Biochemical and Biophysical Research Communications, 2004, 315, 485-492.	2.1	11
32	Overexpression, purification, and biochemical characterization of GumC, an enzyme involved in the biosynthesis of exopolysaccharide by Xylella fastidiosa. Protein Expression and Purification, 2004, 34, 223-228.	1.3	6
33	ESTs as a source for sequence polymorphism discovery in sugarcane: example of the Adh genes. Theoretical and Applied Genetics, 2003, 106, 190-197.	3.6	63
34	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. Genome Research, 2003, 13, 2725-2735.	5.5	254
35	Comparative Analyses of the Complete Genome Sequences of Pierce's Disease and Citrus Variegated Chlorosis Strains of Xylella fastidiosa. Journal of Bacteriology, 2003, 185, 1018-1026.	2.2	307
36	The libraries that made SUCEST. Genetics and Molecular Biology, 2001, 24, 1-7.	1.3	146

#	Article	IF	CITATIONS
37	Expression of sugarcane genes induced by inoculation with Gluconacetobacter diazotrophicus and Herbaspirillum rubrisubalbicans. Genetics and Molecular Biology, 2001, 24, 199-206.	1.3	71
38	Fastidian gum: theXylella fastidiosaexopolysaccharide possibly involved in bacterial pathogenicity. FEMS Microbiology Letters, 2001, 203, 165-171.	1.8	90
39	Trimming and clustering sugarcane ESTs. Genetics and Molecular Biology, 2001, 24, 17-23.	1.3	49
40	The mitochondrial genome of the primary screwworm fly Cochliomyia hominivorax (Diptera:) Tj ETQq0 0 0 rgBT /	Overlock	10 Tf 50 622 1

41	The genome sequence of the plant pathogen Xylella fastidiosa. Nature, 2000, 406, 151-157.	27.8	827